OATS: A STANDARDIZED SYSTEM OF NOMENCLATURE FOR GENES AND CHROMOSOMES AND CATALOG OF GENES GOVERNING CHARACTERS

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Oats: A Standardized System Of Nomenclature For Genes And Chromosomes And Catalog Of Genes Governing Characters

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INTRODUCTION

In 1966, a set of rules for symbolization of genes governing characters in oats and a list of genes were published by a committee that had been assigned this task (Simons, Zillinsky, and Jensen, *1966*).[3] This publication emphasized the need for a unified system, and noted that standardized systems of genetic nomenclature had been established for corn (Emerson, Beadle, and Fraser, *1935*), barley (Robertson, Wiebe, and Immer, *1941*), and wheat (Ausemus, Harrington, Reitz, and Worzella, *1946*). These and other reports on gene nomenclature were studied before the rules for oat genes were adapted from the guide by the International Committee on Genetic Symbols and Nomenclature (Tanaka *et al.*, *1957*).

Experience has shown that this system is basically sound. It can be used with ease by people who are interested in the facets of basic and applied genetics of oats. Since publication of the original set of rules and list of genes, however, several errors have been noted, and many new genes have been discovered. Evidence shows that the rules needed certain minor revisions and some expansion to cover additional aspects of oat genetics. Also, new or revised systems, reflecting new developments and concepts in the field, have been published or proposed for wheat (Kimber and Sears, *1968;* McIntosh, *1973*), and for barley (Ramage, *1972*).

With these thoughts in mind, a second committee, consisting of the authors, was formed, and this publication is the result of their work.

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[3]Authors and year of publication (italic) in parentheses refer to References, p. 24.

RULES FOR SYMBOLIZING GENES AND CHROMOSOMES OF OATS

The rules for oat gene nomenclature published in 1966 (Simons, Zillinsky, and Jensen, *1966*) were based on the report (Tanaka *et al., 1957*) of a committee appointed by the Permanent International Committee for Genetics Congresses. The general rules established by the Tanaka Committee remain as the basic guide to the rules for oat gene nomenclature. Rules for nomenclature of aneuploids in wheat were established by Kimber and Sears (*1968*). A summary of the most applicable of these rules, adapted for oats, also is included in our list of rules. (The original publication should be consulted when additional details or examples of the symbolization of aneuploids are needed.)

1. Symbols of genes, derived from the English name of the character involved or from the Latin name of the organism, as in the case of reaction to a pathogen or insect, will be written in Roman letters. The basic symbol will begin with a capital letter, and, with the exception of genes for reaction to living organisms, this symbol will stand for the dominant allele where only two alleles, one dominant, are known. A recessive allele may be indicated by starting the symbol with a small letter. Symbols for all alleles for reaction to living organisms will start with a capital letter (see rule 2). Each symbol will be short, suggestive, different from all other symbols used for oat genes, and contain not more than one capital letter.

2. Two or more genes governing expression of the same character, or otherwise conditioning phenotypically similar effects, will be designated by a common basic symbol. This means that all genes governing reaction to a specific disease organism, without reference to races of the pathogen or cultivars of the host, will have the same basic symbol. Similarly, all genes governing electrophoretically detectable isozymes of the same enzyme will have the same basic symbol. Within a basic symbol, nonallelic loci will be distinguished by an Arabic numeral on the same line after a hyphen following the basic symbol. The first locus discovered for a character will be assigned the number 1, the second 2, and so on. Members of allelic series will be distinguished by small letters that follow immediately after the locus number. The letters a and b will refer to the original allele-pair. For alleles governing reaction to living organisms, the letter a will refer to the allele conditioning resistance and b for the allele conditioning susceptibility, regardless of dominance relationships.

3. Genes identified by use of aneuploids will be given symbols on the same basis as any other genes. Descriptions of such genes will indicate that they were identified by means of aneuploidy and include monoeffect and nullieffect, where appropriate.

4. Inhibitors, suppressors, enhancers, lethals, and sterility genes will be designated, by the symbols I, Su, En, L, and S, or if they are recessive,

i, su, en, l, and s followed by a hyphen and the symbol of the gene affected.

5. No "wild type" will be recognized as a standard type, and genes occurring in diploid, tetraploid, and hexaploid species will be included in a single system.

6. Linkage groups and corresponding chromosomes will be designated by Arabic numerals.

7. Genic formulas will be written as fractions, with the maternal alleles written as numerators. Each fraction will correspond to a single linkage group. Different linkage groups written in numerical sequence are separated by semicolons. Symbols of unlocated genes will be placed within parentheses at the end of the formula. In euploids and aneuploids, the gene symbols will be repeated as many times as there are homologous loci.

8. Symbols of extrachromosomal factors will be enclosed within brackets and will precede the formula.

9. Chromosomal aberrations will be indicated by abbreviations: Df for deficiency, Dp for duplication, In for inversion, T for translocation, and Tp for transposition. A summary of rules specifically for nomenclature of aneuploids are:

a. Complete chromosomes will be designated by Arabic numerals. This rule will apply to chromosomes paired in homologous bivalents, trivalents or other multivalents, and also in the unpaired monosomic condition.

b. Telocentric chromosomes will be designated by the letter t, whether or not the telocentric chromosome is involved in a pairing configuration. If the telocentric chromosome is paired with a complete chromosome, the telocentric designation will precede the complete chromosome designation.

c. Isochromosomes will be designated by the small letter i, whether or not the isochromosome is involved in a pairing configuration.

d. Nullisomics will be indicated by the symbol O, followed by the symbols indicating which chromosome is absent.

e. The ability of chromosomes to pair will be indicated by superscripts following the chromosome symbols. For example, a euploid plant of *Avena sativa* will be designated as $21''$, and a monosomic deficiency as $20'' + 1'$.

f. At the time this is being written, there is no consensus among different investigators regarding numbering schemes for the chromosome complement. Therefore, rules on designation of chromosomes are being delayed until a standard numbering system can be devised.

10. The zygotic number of chromosomes will be indicated by 2n, the gametic number by n, and the basic number by x.

OAT GENES AND ASSIGNED SYMBOLS

A survey of literature reporting genetic studies of oats attempted to determine which reports duplicated the discoveries of earlier investigators. This often necessitated making more or less arbitrary decisions. In general, for genes governing disease reaction, a gene reported by second and subsequent investigators in the same or obviously related cultivars was assumed the same as the gene first reported in that cultivar for that character unless a different gene was evident. Genes conditioning the same basic character, but reported from unrelated cultivars, were assumed to be neither identical nor allelic unless there were some reason.

For genes of characters other than disease reaction, genes governing expression of the same character were assumed identical if they were reported from oats having the same genome constitution, unless there were some reason to think otherwise.

The genes, or loci, recognized are listed alphabetically by symbol. The reference given after each symbol is usually, but not always, the earliest reported discovery of the gene based on the committee's investigations. References listed after the description report additional studies of the gene or pertain to genes now tentatively regarded as the same gene. Future investigations or a more critical examination of existing data may show that some of these reports actually dealt with distinct genes. When this occurs, such genes will be assigned their own numbers. Descriptions, symbols, and pages on which they appear follow:

Gene Symbol	Reference and description
A-1.	Norton (*1907*). Gene conditioning awnedness in cultivated hexaploid oats. Dominance and expressivity variable. Nilsson-Ehle (*1914*), Surface (*1916*), Zinn and Surface (*1917*), Love and Fraser (*1917*), Wilds (*1917*), Love and Craig (*1918b*), Fraser (*1919*), Henning (*1924*), Reed and Stanton (*1925*), Cotner (*1929*), Tschermak (*1929*), Shaw and Bose (*1933*), Philp (*1933*), Johnson (*1933*), Aamodt *et al.* (*1934*), De Villiers (*1935*), Tang (*1938*), Torrie (*1939*), Ko *et al.* (*1946*), Coffman (*1964*).

A-2. Zade (*1912*). Gene conditioning awnedness in wild hexaploid oats. Dominance and expressivity variable. Possibly pleiotropic for basal articulation. Surface (*1916*), Love and Fraser (*1917*), Wilds (*1917*), Love and Craig (*1918b*), Tschermak (*1929*), Philp (*1933*), Aamodt *et al.* (*1934*).

A-3. Wiggans (*1918*). A second gene conditioning awnedness in wild hexaploid oats. Dominance and expressivity variable. Possibly pleiotropic for basal articulation. Reed and Stanton (*1925*), Tschermak (*1929*), Coffman (*1964*).

A-4. Jones (*1940*). Gene conditioning awnedness in diploid and tetraploid oats. Possibly pleiotropic for basal articulation. Dyck (*1966*).

A-5. Nishiyama (*1933*). Gene for absence of awns on primary and secondary floret. Discovered by monosomic analysis.

ap-1. Tang (*1938*). Recessive gene conditioning awn pubescence in strains of *A. sterilis macrocarpa.*

Ba-1. Surface (*1916*). A generally partly dominant gene conditioning the "cultivated" type of basal articulation of the primary floret in crosses with species and varieties having "wild" type basal articulation. Wilds (*1917*), Wiggans (*1918*), Love and Craig (*1918b*), Fraser (*1919*), Henning (*1924*), Coffman *et al.* (*1925*), Goulden (*1926*), Tschermak (*1929*), Ma (*1933*), Philp (*1933*), Shaw and Bose (*1933*), Aamodt *et al.* (*1934*), Middleton (*1938*), Tang (*1938*), Hayes *et al.* (*1939*), Torrie (*1939*), Ko *et al.* (*1946*), Kehr and Hayes (*1950*), Day (*1963*), Coffman (*1964*).

Ba-2. Tschermak (*1929*). Second gene conditioning "cultivated" type of basal articulation of the primary floret in crosses between *A. sativa,* and between *A. fatua* and *A. sterilis.*

Ba-3. Ko *et al.* (*1946*). Gene conditioning "cultivated" type of basal articulation of the primary floret in SD334, complementary with Ba-4.

Ba-4. Ko *et al.* (*1946*). Gene conditioning "cultivated" type of basal articulation of the primary floret in SD334, complementary with Ba-3.

Ba-5. Jones (*1940*). Dominant gene conditioning "wild" type basal articulation of the primary floret in diploid and tetraploid species of *Avena,* complementary with Ba-6. Designated "X."

Ba-6. Jones (*1940*). Second dominant gene conditioning "wild type" basal articulation of the primary floret in diploid and tetraploid species of *Avena,* complementary with Ba-5. Designated "Y."

Ba-7. Nishiyama (*1973*). Gene for wild type of basal articulation of primary and secondary florets, in progeny of *A. barbata* x *A. strigosa.* Designated "W."

Ba-8. Nishiyama (*1973*). Complementary gene conditioning, with ba-7b, basifracture of the secondary floret, hypostatic to Ba-7, in progeny of *A. barbata* x *A. strigosa.* Designated "B."

Ba-9. Nishiyama (*1933*). Dominant gene for the cultivated type of basal articulation of the primary and secondary floret. Discovered by monosomic analysis.

Bl-1. Mackie (*1928*). Partly dominant gene for resistance to blast in Kanota.

cda-1. Nishiyama (*1941*). Gene for chlorophyll deficiency-albino, linked to ma-1 and L-1, in progeny of *A. barbata* x *A. strigosa.* Designated "al," "G," and "C." Nishiyama (*1934*).

cda-2. Nishiyama (*1957*). Gene for chlorophyll deficiency-albino, linked to Lp-9 and Lc-12, in progeny of *A. barbata* x *A. strigosa.*

cda-3. Smith (*1938*). Recessive gene for chlorophyll deficiency-albino found in progeny of Victoria.

Cda-4. McGinnis and Taylor (*1961*). Gene for normal chlorophyll production (nullieffect). ST chr 21 (Rajhathy's karyotype, *1963*). McGinnis *et al.* (*1963*).

Cda-5. McGinnis and Andrews (*1962*). Gene for normal chlorophyll production (nullieffect). SM chr 15 (Rajhathy's karyotype, *1963*).

Cda-6. McGinnis (*1966*). Gene for normal chlorophyll production (nullieffect) reported by Dyck and Rajhathy (*1965*). McGinnis *et al.* (*1968*).

cdc-1. Åkerman and Froier (*1941*). Gene conditioning chlorophyll deficiency-chlorina in Golden Rain. Designated "Chlor 1." Froier (*1946*), Morey and Earhart (*1952*).

cdc-2. Åkerman and Froier (*1941*). Gene conditioning chlorophyll deficiency-chlorina in Golden Rain. Designated "Chlor 2." Froier (*1946*).

cdc-3. Åkerman and Froier (*1941*). Gene conditioning chlorophyll deficiency-chlorina in Golden Rain. Designated "Chlor 3." Froier (*1946*).

cdc-4. Nishiyama (*1957*). Recessive gene for yellow plant color, in progeny of *A. barbata* x *A. strigosa.*

cdl-1. Froier (*1946*). Gene conditioning chlorophyll deficiency-lutescens in Novahavre. Designated "Lp." Åkerman (*1922*).

cdl-2. Froier (*1946*). Second gene conditioning chorophyll deficiency-lutescens in Novahavre. Designated "Ln." Åkerman (*1922*).

cdl-3. Froier (*1946*). Gene conditioning chlorophyll deficiency-lutescens in the variety Swedish. Designated "Ls." Åkerman (*1922*).

cdn-1. Chang and Sadanaga (*1964*). Gene conditioning chlorophyll deficiency-netting in A 382-91-2, on Monosome A. Designated "nt-1."

cdn-2. Chang and Sadanaga (*1964*). Gene conditioning chlorophyll deficiency-netting in A 382-91-2.

cds-1. Coffman (*1964*). Gene conditioning chlorophyll deficiency-stripe (yellow) in Burt.

cds-2. Coffman (*1964*). Second gene conditioning chlorophyll deficiency-stripe (yellow) in Burt.

cds-3. Coffman (*1964*). Third gene conditioning chlorophyll deficiency-stripe (yellow) in Burt.

cdv-1. Froier (*1948*). Gene conditioning chlorophyll deficiency-albovirescens. Abrams *et al.* (*1964*).

Dd-1. Griffiths and Holden (*1957*). Dominant gene carried by Gray Winter for resistance to the stem eelworm, *Ditylenchus dipsaci* (Kühn). Filipjev.

dw-1. Warburton (*1919*). Recessive gene conditioning grassy dwarfness in plants derived from Victory.

Dw-2. Stanton (*1923*). Gene for semidwarfness in progeny of Winter Turf x Sixty Day. Designated "D." Cotner (*1929*), Florell (*1931*), Litzenberger (*1949b*).

Dw-3. Stanton (*1923*). Gene for semidwarfness in progeny of Aurora x Pringle Progress. Cotner (*1929*), Florell (*1931*), Litzenberger (*1949b*).

Dw-4. Derick (*1930*). Gene for semidwarfness in Trelle Dwarf. Patterson *et al.* (*1963*).

dw-5. Nishiyama (*1957*). Recessive gene for dwarfness, in progeny of *A. barbata* x *A. strigosa.*

Dw-6. Brown and McKenzie (*1976*).[4] A completely dominant gene for dwarfness in a Harmon derivative induced by irradiation.

E-1. Marshall and Allard (*1969*). Gene for esterase in certain strains of *Avena barbata.* Designated "E_4."

E-2. Marshall and Allard (*1969*). Gene for esterase in certain strains of *Avena barbata.* Designated "E_9."

E-3. Marshall and Allard (*1969*). Gene for esterase in certain strains of *Avena barbata.* Designated "E_{10}."

Eg-1. Jones and Griffiths (*1952*). Gene for resistance to *Erysiphe graminis* DC. in Cc4146.

Eg-2. Jones and Griffiths (*1952*). Gene for resistance to *Erysiphe graminis* in *A. strigosa.*

[4]Personal communication.

Eg-3. Hayes and Jones (*1966*). Gene for resistance to races 2 and 3 of *Erysiphe graminis* in Cc4347.

Eg-4. Thomas, Leggett, and Jones (*1975*). Gene for resistance to all currently prevalent races of *Erysiphe graminis* in *Avena barbata* Cc4897. Was transferred to *A. sativa* Manod.

Fd-1. Wiggans (*1918*). Gene for type of secondary floret disjunction. Henning (*1924*), Cotner (*1929*), Tschermak (*1929*), Florell (*1931*), Ma (*1933*), Torrie (*1939*), Hayes *et al.* (*1939*), Ko *et al.*(*1946*), Coffman (*1964*).

Fd-2. Ko *et al.* (*1946*). Second gene for type of secondary floret disjunction. See "Fd-1" for possible additional references.

fl-1. Dyck (*1968*). Recessive gene affecting the normal development of florets of *A. strigosa* spikelets are completely lacking on plants of this mutant.

I-Ft-1. Huskins (*1927*). Gene that inhibits the expression of fatuoid characters (nullieffect). Heterozygote fatuoid (monoeffect). Nishiyama (*1931*), Hacker and Riley (*1965*), Singh and Wallace (*1967*), Thomas and Mytton (*1970*), Chang and Sadanaga (*1964*).

Gf-1. Nishiyama (*1973*). Gametophyte gene effecting preferential fertilization of pollen, in progeny of *A. barbata* x *A. strigosa*. Designated "g."

Gi-1. Zhegalov (*1920*). Dominant gene for giantism in *A. orientalis.*

gi-2. Zillinsky (*1959*). Recessive gene ("monster") for giantism in progeny of Clintland-Garry x Laurel-Klein 69B.

Ha-1. Andersen (*1961*). Gene in Grise de Houdan for resistance to the cereal root eelworm, *Heterodera avenae* Woll.

Ha-2. Andersen (*1961*). Dominant gene in certain American oat varieties for resistance to the cereal root eelworm, *Heterodera avenae* Woll.

Ha-3. MacKey (*1975*).[5] Gene for resistance to the oat cyst nematode (*Heterodera avenae* Filipjev) derived from the *Avena sterilis* cv. Ronda.

Hv-1. Murphy and Meehan (*1946*). Dominant gene in Victoria for susceptibility to Victoria blight, caused by *Helminthosporium victoriae* Meehan and Murphy. May be pleiotropic or closely linked to Pc-2. Litzenberger (*1949a*), Finkner (*1953*), Welsh *et al.* (*1954*).

kn-1. Gauthier and McGinnis (*1965*). Gene for normal peduncle (kneck) development (nullieffect—distinct kinking of the neck). Hacker and Riley (*1965*).

[5]Personal communication.

Kp-1. Nilsson-Ehle (*1908*). Gene for long hairs (kernel pubescence) at base of kernel. Zinn and Surface (*1917*).

Kp-2. Nilsson-Ehle (*1908*). Gene for short hairs (kernel pubescence) at base of kernel. Zinn and Surface (*1917*).

Kp-3. Zade (*1912*). Gene for heavy kernel pubescence in *A. fatua.* Wilds (*1917*), Tschermak (*1929*), Jones (*1930*), Federova (*1930*), Philp (*1933*), Aamodt *et al.* (*1934*).

Kp-4. Wiggans (*1918*). Gene for kernel pubescence in Red Texas. Fraser (*1919*), Schafer (*1923*), Henning (*1924*), Cotner (*1929*), Shaw and Bose (*1933*), Ma (*1933*), Tang (*1938*), Middleton (*1938*), Torrie (*1939*), Hayes *et al.* (*1939*), Ko *et al.* (*1946*), Litzenberger (*1949b*), Kehr and Hayes (*1950*), Craigmiles (*1952*), Coffman (*1964*).

Kp-5. Wiggans (*1918*). Second gene for kernel pubescence in Red Texas. Shaw and Bose (*1933*), Tang (*1938*).

Kp-6. Henning (*1924*). Gene for dense kernel pubescence in *A. sterilis nigra.*

Kp-7. Federova (*1930*). Gene modifying kernel pubescence. Designated "m_1." Ma (*1933*).

Kp-8. Federova (*1930*). Second gene modifying kernel pubescence. Ma (*1933*).

Kp-9. Ko *et al.* (*1946*). Complementary gene conditioning, with Kp-10, kernel pubescence in cross between Bond and SD334.

Kp-10. Ko *et al.* (*1946*). Complementary gene conditioning, with Kp-9, kernel pubescence in cross between Bond and SD334.

Kp-11. Nishiyama (*1933*). Gene for glabrous base of primary and secondary floret. Discovered by monosomic analysis.

1-1. Nishiyama (*1934*). Lethal gene, linked to Ma-1 and Cda-1, in progeny of *A. barbata* x *A. strigosa.* Nishiyama (*1941*).

1-2. Nishiyama (*1934*). Lethal gene, linked to Ba-7, in progeny of *A. barbata* x *A. strigosa.* Designated "1." Nishiyama (*1973*).

Lc-1. Wilson (*1904*). Incompletely dominant gene for black or dark lemma color. Norton (*1907*), Wilson (*1907*), Nilsson-Ehle (*1909*), Surface (*1916*), Zinn and Surface (*1917*), Wilds (*1917*), Love and Craig (*1918b*), Caporn (*1918*), Wakabayashi (*1921*), Gaines (*1924*), Quisenberry (*1926*), Meurman (*1927*), Garber and Quisenberry (*1928*), Hayes *et al.* (*1928*), Odland (*1928*), Federova (*1930*), Welsh (*1931*), Florell (*1931*), Robb (*1932*), Ru (*1933*), Johnson (*1933*), Philp (*1933*), Ma (*1933*), Aamodt *et al.* (*1934*), De Villiers (*1935*), Åkerman and Bader (*1937*), Tang (*1938*), Middleton (*1938*), Patel (*1941*), Åkerman (*1948*), Coffman (*1964*).

Lc-2. Nilsson-Ehle (*1909*). Gene for gray lemma color expressed only in the absence of black. Designated "Gr." Surface (*1916*), Wilds (*1917*), Love and Craig (*1918b*), Caporn (*1918*), Henning (*1924*), Meurman (*1927*), Federova (*1930*), Welsh (*1931*), Robb (*1932*), Johnson (*1933*), Philp (*1933*), Ma (*1933*), Aamodt *et al.* (*1934*), Coffman (*1964*).

En-Lc-2. Meurman (*1927*). Gene that intensifies gray lemma color in the presence of Lc-2. Designated "Z."

Lc-3. Nilsson-Ehle (*1909*). Second gene for black lemma color. Designated "S_2." Robb (*1932*), Akerman (*1948*), Coffman (*1964*).

Lc-4. Nilsson-Ehle (*1909*). Gene for yellow lemma color. Designated "G." Surface (*1916*), Wilds (*1917*), Love and Craig (*1918b*), Fraser (*1919*), Cotner (*1929*), Ma (*1933*), Torrie (*1939*), Coffman (*1964*).

Lc-5. Fraser (*1919*). Second gene for yellow lemma color. Designated "Y."

Lc-6. Fraser (*1919*). Gene for red lemma color. Designated "R." Schafer (*1923*), Henning (*1924*), Cotner (*1929*), Torrie (*1939*), Ko *et al.* (*1946*), Coffman (*1964*).

Lc-7. Cotner (*1929*). Second gene for red lemma color. Coffman (*1964*).

Lc-8. Welsh (*1931*). Dominant gene for white lemma color.

Lc-9. Welsh (*1931*). Second dominant gene for white lemma color.

Lc-10. Ko *et al.* (*1946*). Complementary gene conditioning, with Lc-11, white to yellowish lemma color.

Lc-11. Ko *et al.* (*1946*). Complementary gene conditioning, with Lc-10, white to yellowish lemma color.

Lc-12. Nishiyama (*1934*). Gene for light-brown lemma color, dominant over gray lemma color of *A. strigosa,* linked to Lp-9 and cda-2, in progeny of *A. barbata* x *A. strigosa.* Designated "B1." Nishiyama (*1957*).

Lf-1. Finkner, Murphy, Atkins, and West (*1954*). Dominant gene for lemma fluorescence under UV. Designated "F." May be associated with lemma color.

Lf-2. Finkner, Murphy, Atkins, and West (*1954*). Second dominant gene for lemma fluorescence under UV. Designated "L." May be associated with lemma color.

Lg-1. Nilsson-Ehle (*1909*). Dominant gene for presence of ligule in open panicle oats. Designated "L_1." Love and Craig (*1918a*), Garber (*1922*), Meurman (*1927*), Odland (*1928*), Akerman and Muhlow (*1933*).

Lg-2. Nilsson-Ehle (*1909*). Second dominant gene for presence of ligule in open panicle oats. Designated "L_2." Love and Craig (*1918a*), Garber (*1922*), Meurman (*1927*), Odland (*1928*), Akerman and Muhlow (*1933*).

Lg-3. Nilsson-Ehle (*1909*). Third dominant gene for presence of ligule in open panicle oats. Designated "L_3." Meurman (*1927*), Åkerman and Muhlow (*1933*).

Lg-4. Nilsson-Ehle (*1909*). Fourth dominant gene for presence of ligule in open panicle oats. Designated "L_4."

ln-1. Sadanaga (*1971*). Recessive gene conditioning leaf necrosis, which is temperature sensitive.

Lp-1. Bartlett (*1916*). Dominant gene for lemma pubescence in *A. fatua*. Surface (*1916*), Wilds (*1917*), Love and Craig (*1918b*), Federova (*1930*), Florell (*1931*), Ma (*1933*), Philp (*1933*), Aamodt *et al.* (*1934*), De Villiers (*1935*).

I-Lp-1. Barlett (*1916*). Gene inhibiting expression of Lp-1. Love and Craig (*1918b*), Federova (*1930*), Ma (*1933*), De Villiers (*1935*).

Lp-2. Wilds (*1917*). Second dominant gene for lemma pubescence in *A. fatua*. Philp (*1933*).

Lp-3. Cotner (*1929*). Gene for Lemma pubescence in *A. sterilis*. Tang (*1938*).

Lp-4. Cotner (*1929*). Second gene for lemma pubescence in *A. sterilis*. Tang (*1938*).

Lp-5. Tang (*1938*). Third gene for lemma pubescence in *A. sterilis*.

Lp-6. Nishiyama (*1934*). Gene for prostrate hairs of lemma, dominant over glabrous in progeny of *A. barbata* x *A. strigosa*. Designated "P_1."

Lp-7. Nishiyama (*1934*). Complementary gene conditioning, with Lp-6 and Lp-8, erect hairs on lemma, in progeny of *A. barbata* x *A. strigosa*. Designated "C."

Lp-8. Nishiyama (*1934*). Complementary gene conditioning, with Lp-6 and Lp-7, erect hairs on lemma, in progeny of *A. barbata* x *A. strigosa*. Designated "E."

Lp-9. Nishiyama (*1957*). Dominant gene for slight pubescence on lemma, linked to Lc-12 and cda-2, in progeny of *A. barbata* x *A. strigosa*. Designated "P_2."

Lw-1. Nilsson-Ehle (*1908*). Gene for lemma waxiness. Meurman (*1927*).

Ma-1. Nishiyama (*1941*). Dominant gene for early maturity, linked to Cda-1 and 1-1, in progeny of *A. barbata* x *A. strigosa*. Designated "Re."

mg-1. Dyck (*1968*). Recessive gene conditioning complete sterility, with floral parts replaced by a series of glumes, in *Avena strigosa*.

ms-1. Nishiyama (*1957*). Recessive gene for male sterility in progeny of *A. barbata* x *A. strigosa*. Meiosis usually stops at diakinesis.

ms-2. Sadanaga (*1965*). Recessive gene for partial male sterility in X-irradiated Saia (*Avena strigosa*).

N-1. Norton (*1907*). Gene, with variable dominance, conditioning naked seed and multiflorous spikelet. Tschermak (*1910*), Gaines (*1917*), Zinn and Surface (*1917*), Caporn (*1918*), Love and McRostie (*1919*), Reed (*1925*), Lebedeff (*1930*), Chou (*1932*), Clamont (*1969*), Moule (*1972*), Boland and Lawes (*1972*), Atiyya and Williams (*1976*).

N-2. Moule (*1972*). Secondary gene that modifies the expression of the N-1 gene.

N-3. Moule (*1972*). Further secondary gene that modifies the expression of the N-1 gene.

nh-1. Nishiyama (*1934*). Recessive gene for nonheading, in progeny of *A. barbata* x *A. strigosa.* Nishiyama (*1957*).

Np-1. Florell (*1931*). Gene for nodal pubescence in *A. sterilis* and *A. byzantina.* Litzenberger (*1949a*), Craigmiles (*1952*).

P-1. Marshall and Allard (*1969*). Gene for phosphatase in certain strains of *Avena barbata.* Designated "P_5."

Pc-1. Davies and Jones (*1927*). Dominant gene for resistance to crown rust, caused by *Puccinia coronata* Cda. var. *avenae* Fraser and Led., in Red Rustproof. Designated "S" by Dietz and Murphy (*1930*).

I-Pc-1. Dietz and Murphy (*1930*). Dominant gene inhibiting Pc-1. Designated "I."

Pc-2. Murphy *et al.* (*1937*). Partially dominant gene for resistance to *P. coronata* race 1 in Victoria. Is pleiotropic or closely linked with Hv-1. Waterhouse (*1939*), Weetman (*1942*), Cochran *et al.* (*1945*), Murphy and Meehan (*1946*), Litzenberger (*1949b*), Vallega (*1951*), Finkner (*1953*), Griffiths (*1953*), Finkner (*1954*), Welsh *et al.* (*1954*), Simons (*1956*), Craigmiles (*1956*), Chang (*1959*), Chang and Sadanaga (*1964*).

Pc-2b. Finkner (*1954*). Gene for resistance to *P. coronata* race 57 in Anthony-Bond x Boone. Designated "V_1" and is not associated with susceptibility to *Helminthosporium victoriae.*

Pc-3. Hayes *et al.* (*1939*). Complementary gene conditioning, with Pc-4, resistance to *P. coronata* in Bond. Torrie (*1939*), Weetman (*1942*), Cochran *et al.* (*1945*), Ko *et al.* (*1946*), Litzenberger (*1949b*), Kehr and Hayes (*1950*), Griffiths (*1953*), Šebesta (*1976*).

Pc-3c. Weetman (*1942*). Complementary gene conditioning, with Pc-4c, resistance to some isolates of *P. coronata* race 1 in Ukraine. Upadhyaya and Baker (*1962b*).

I-Pc-3. Cochran *et al.* (*1945*). Dominant gene in Richland-Fulghum that inhibits Pc-3. Designated "C."

Pc-4. Hayes *et al.* (*1939*). Complementary gene conditioning, with Pc-3, resistance to *P. coronata* in Bond. Torrie (*1939*), Weetman (*1942*), Cochran *et al.* (*1945*), Ko *et al.* (*1946*), Litzenberger (*1949b*), Kehr and Hayes (*1950*), Griffiths (*1953*), Šebesta (*1976*).

Pc-4c. Weetman (*1942*). Complementary gene conditioning, with Pc-3b, resistance to some isolates of *P. coronata* race 1 in Ukraine. Upadhyaya and Baker (*1962b*).

I-Pc-4. Cochran *et al.* (*1945*). Dominant gene in Richland-Fulghum that inhibits Pc-4. Designated "D."

Pc-5. Litzenberger (*1949a*). Dominant gene for resistance to *P. coronata* races 1 and 45 in Landhafer. Kehr and Hayes (*1950*), Finkner (*1954*), Simons and Murphy (*1954*), Baker (*1955*), Craigmiles (*1956*), Chang (*1959*), Rivers (*1959*), Upadhyaya and Baker (*1962b*), Patterson *et al.* (*1963*), Chang and Sadanaga (*1964*).

Pc-6. Litzenberger (*1949b*). Dominant gene for resistance to *P. coronata* races 1 and 45 in Santa Fe. Designated "S." Osler and Hayes (*1953*) designated it "S"; Finkner (*1954*) designated it "M_1"; Simons and Murphy (*1954*), Baker (*1955*), Finkner *et al.* (*1955*), Craigmiles (*1956*), and Chang (*1959*) designated it "M." Upadhyaya and Baker (*1962b*).

Pc-6c. Finkner (*1954*). Dominant gene for resistance to *P. coronata* race 57 in Ukraine. Designated "M" and is linked to Pc-9. Finkner *et al.* (*1955*), Sanderson (*1960*), Upadhyaya and Baker (*1962b*).

Pc-6d. Finkner (*1954*). Dominant gene for resistance to *P. coronata* race 57 in Trispernia and Anthony-Bond x Boone. Designated "M_2." Simons and Murphy (*1954*), Baker (*1955*), Craigmiles (*1956*), Upadhyaya and Baker (*1962b*).

Pc-7. Osler and Hayes (*1953*). Complementary gene conditioning, with Pc-8, resistance to *P. coronata* races 45 and 57 in Santa Fe. Designated "D."

Pc-8. Osler and Hayes (*1953*). Complementary gene conditioning, with Pc-7, resistance to *P. coronata* races 45 and 57 in Santa Fe. Designated "D."

Pc-9. Finkner (*1954*). Second dominant gene for resistance to *P. coronata* race 57 in Ukraine. Designated "U" and is linked to Pc-6c. Finkner *et al.* (*1955*), Sanderson (*1960*), Upadhyaya and Baker (*1962b*).

Pc-9c. Simons and Murphy (*1954*). Gene for resistance to *P. coronata* races 45 and 101 in a derivative of Santa Fe. It is linked to Pc-6. Finkner *et al.* (*1955*) designated it "U," and Chang (*1959*) used the same symbol.

Pc-10. Finkner (*1954*). Dominant gene for resistance to *P. coronata* race 57 in Klein 69B. Designated "K." Sanderson (*1960*).

I-Pc-10. Finkner (*1954*). Dominant gene in Clinton inhibiting Pc-10. Designated "I_k."

Pc-11. Welsh *et al.* (*1954*). Dominant gene for resistance to *P. coronata* races 1 and 45 in Victoria. Waterhouse (*1939*), Vallega (*1951*), Chang and Sadanaga (*1964*).

Pc-12. Welsh *et al.* (*1954*). Second dominant gene for susceptibility to *P. coronata* races 1 and 45 in Victoria.

Pc-13. Finkner *et al.* (*1955*). Dominant gene for resistance to *P. coronata* race 109 in Clinton. Designated "A." Chang (*1959*) designated it "b^R."

Pc-13c. Chang (*1959*). Gene for susceptibility to *P. coronata* race 258 De Argelia and Dom Pedrito. Designated "B."

Pc-13d. Chang (*1959*). Second gene for susceptibility to *P. coronata* race 258 De Argelia and Dom Pedrito. Designated "b."

I-Pc-13. Chang (*1959*). Dominant gene inhibiting Pc-13, in Gopher and other lines.

Pc-14. Simons (*1956*). Dominant gene for resistance to *P. coronata* race 202 in Ascencao. Designated "E." Chang (*1959*).

I-Pc-14. Chang (*1959*). Dominant gene inhibiting Pc-14, in Gopher and other lines. Designated "I_E."

Pc-15. Murphy *et al.* (*1958*). Dominant gene for resistance to *P. coronata* races 202 and 258 in the diploid Saia. Simons *et al.* (1959), Marshall and Myers (*1961*), Dyck and Zillinsky (*1962*), Dyck and Zillinsky (*1963*).

Pc-16. Murphy *et al.* (*1958*). Second dominant gene for resistance to *P. coronata* races 202 and 258 in the diploid Saia. Marshall and Myers (*1961*).

Pc-17. Murphy *et al.* (*1958*). Third dominant gene for resistance to *P. coronata* races 202 and 258 in the diploid Saia.

Pc-18. Simons *et al.* (*1959*). Dominant gene for resistance to *P. coronata* races 205, 216, and 264 in the diploid Glabrota. Marshall and Myers (*1961*).

Pc-19. Simons *et al.* (*1959*). Dominant gene for resistance to *P. coronata* races 205, 227, and 264 in the diploid C.I. 3815. Marshall and Myers (*1961*).

Pc-20. Simons *et al.* (*1959*). Gene for resistance to *P. coronata* races 202, 203, 205, 216, and 264 in the tetraploid C.I. 7233.

Pc-21. Chang (*1959*). Gene for resistance to *P. coronata* races 203, 216, and 258 in Santa Fe. Designated "S."

Pc-22. McKenzie (*1961*). Incompletely dominant gene for resistance to *P. coronata* races 264, 279, and 290 in Ceirch dubach.

Pc-23. Dyck and Zillinsky (*1963*). Gene for resistance to *P. coronata* race 264 (but not race 294) in the diploid C.D. 3820.

Pc-24. Upadhyaya and Baker (*1960*). Complementary dominant gene conditioning resistance, with Pc-25, to *P. coronata* races 203, 226, 230, 237, and 286 in Garry. Designated "Vc_a." Upadhyaya and Baker (*1962b*).

Pc-25. Upadhyaya and Baker (*1960*). Complementary dominant gene conditioning resistance, with Pc-24, to *P. coronata* races 203, 226, 230, 237, and 286 in Garry. Designated "Vc_b." Upadhyaya and Baker (*1962b*).

Pc-26. Upadhyaya and Baker (*1960*). Gene for resistance to *P. coronata* in Garry. Designated "Vc_2." Upadhyaya and Baker (*1962b*).

I-Pc-26. Upadhyaya and Baker (*1960*). Gene inhibiting Pc-26. Designated "IVc_2."

Pc-27. Upadhyaya and Baker (*1960*). Gene for adult resistance to *P. coronata* in Garry. Designated "Vc_1." Upadhyaya and Baker (*1962b*).

Pc-28. Upadhyaya and Baker (*1960*). Second gene for adult resistance to *P. coronata* in Garry. Designated "Vc_3." Upadhyaya and Baker (*1962b*).

Pc-29. Marshall and Myers (*1961*). Second gene for resistance to *P. coronata* race 216 in the diploid Glabrota.

Pc-30. Marshall and Myers (*1961*). Second gene for resistance to *P. coronata* races 216 and 276 in the diploid C.I. 3815.

Pc-31. Marshall and Myers (*1961*). Dominant gene for resistance to *P. coronata* races 203, 216, and 276 in the diploid C.I. 4746.

Pc-32. Marshall and Myers (*1961*). Dominant gene for resistance to *P. coronata* races 203, 216, and 276 in the diploid Ceirch Llwyd.

Pc-33. Marshall and Myers (*1961*). Second dominant gene for resistance to *P. coronata* race 216 in the diploid Ceirch Llwyd.

Pc-34. McKenzie and Fleischmann (*1964*). Gene for resistance to *P. coronata* races 203, 205, 264, 276, and 279 in D-60.

Pc-35. McKenzie and Fleischmann (*1964*). Dominant gene for resistance to *P. coronata* races 203, 205, 264, 276, and 279 in *A. sterilis* D-137 collected in Israel. Fleischmann *et al.* (*1971a*). Allelic or closely linked to Pc-54. McKenzie and Martens (*1976*).[6]

Pc-36. Simons (*1965*). Dominant gene for resistance to crown rust races 203, 216, 264, 290, and 321 carried by C.I. 8081 (*A. sterilis* selection from P.I. 267989).

Pc-37. Dyck (*1966*). Dominant gene for resistance to crown rust race 294 carried by diploid C.D. 7994.

Pc-38. Fleischmann and McKenzie (*1968*). Gene carried by *A. sterilis*

[6]Personal communication.

CW491-4 for resistance to crown rust races 264, 290, 295, 332, and 446—susceptible to race 202.

Pc-39. Fleischmann and McKenzie (*1968*). Dominant gene for resistance to *P. coronata* races 264, 290, 295, 332, and 446 in *A. sterilis* F366 collected in Israel. Allelic or closely linked to Pc-55. Kiehn *et al.* (*1976*).

Pc-40. Fleischmann and McKenzie (*1968*). Dominant gene for resistance to *P. coronata* races 290, 295, 332, and 446 in *A. sterilis* F83 collected in Israel.

Pc-41. Fleischmann and McKenzie (*1968*). Gene carried by *A. sterilis* F83 for resistance to crown rust races 290, 295, and 332.

Pc-42. Fleischmann and McKenzie (*1968*). Gene carried by *A. sterilis* F83 for resistance to crown rust race 332 but not 264, 290, 295, or 446.

Pc-43. Fleischmann and McKenzie (*1968*). Gene carried by *A. sterilis* F83 for resistance to crown rust race 290, but not 264, 295, 332, and 446.

Pc-44. Martens, McKenzie, and Fleischmann (*1968*). Dominant gene in Kyto for resistance to crown rust races 210, 228, 239, 297, 330, 341, 342, and 453.

Pc-45. Fleischmann *et al.* (*1971a*). Dominant gene in *A. sterilis* F-169 for resistance to crown rust races 239, 264, 290, 326, 330, and 332.

Pc-46. Fleischmann *et al.* (*1971a*). Dominant gene for resistance to *P. coronata* races 239, 264, 290, 326, 330, and 332 in *A. sterilis* F290 collected in Israel. Allelic or closely linked to Pc-50.

Pc-47. Fleischmann *et al.* (*1971b.*). Dominant gene in C. I. 8081A, for resistance to crown rust, from P.I. 267989-*A. sterilis,* probably identical to Pc-36.

Pc-48. Fleischmann *et al.* (*1971b*). Dominant gene in *A. sterilis* F-158 for resistance to crown rust.

Pc-49. Fleischmann *et al.* (*1971b.*). Dominant gene for resistance to *P. coronata* races 216, 326, 330, 332, and 446 in *A. sterilis* F158 collected in Israel. Subsequent pathological and genetic data (McKenzie and Martens, unpublished) indicate Pc-49 is identical to Pc-40.

Pc-50. Fleischmann *et al.* (*1971b*). Dominant gene for resistance to *P. coronata* races 216, 264, 305, 326, and 330 in *A. sterilis* CW 486 collected in Tunisia. Allelic or closely linked to Pc-46.

Pc-51. Browning (*1971*).[7] Dominant gene for resistance from *A. sterilis,* Wahl No. 8, carried by Iowa Midseason isoline X 270, and early isoline X 434.

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[7]Personal communication.

Pc-52. Browning (*1972*).[8] Dominant gene for resistance from *A. sterilis,* Wahl No. 2, carried by Iowa Midseason isoline X-421.

Pc-53. Simons (*1976*).[8] Single gene, lacking clear dominance, derived from *A. sterilis* 6-112-1-15 via H441.

Pc-54. McKenzie and Martens (*1976*).[8] Incompletely dominant gene for resistance to cultures of *P. coronata* races 239, 264, and 295 in *A. sterilis* CAV 1830 and CAV 1832 collected in Turkey. Allelic or closely linked to Pc-35.

Pc-55. Kiehn *et al.* (*1976*). Incompletely dominant gene for resistance to cultures of *P. coronata* races 203, 211, 239, 259, 264, 295, and 326 in *A. sterilis* CAV 4963 collected in Israel. Allelic or closely linked to Pc-39.

Pc-56. Kiehn *et al.* (*1976*). Gene for crown rust resistance in *Avena sterilis* CAV 1964.

Pc-57. Simons (*1976*).[8] Gene conditioning resistance at high temperatures to crown rust race 264A and many other races. Derived from *A. sterilis* D-94 (C.I. 8295) via H-555.

Pc-58. McDaniel (*1976*).[8] Gene carried by TAM-O-301 for resistance to race 264B and many other races of crown rust. Derived from *Avena sterilis* P.I. 295919 (C.I. 8387).

Pc-59. McDaniel (*1976*).[8] Gene carried by TAM-0-312 for resistance to race 264B and many other races of crown rust. Derived from *Avena sterilis* P.I. 296244 (C.I. 8393).

Pc-60. McDaniel (*1976*).[8] Gene carried by Coker 227 for resistance to many races of crown rust. Derived from *Avena sterilis* P.I. 287211.

Pc-61. McDaniel (*1976*).[8] Gene carried by Coker 234 for resistance to many races of crown rust. Derived from *Avena sterilis* P.I. 287211.

Pg-1. Garber (*1921*). Dominant gene for resistance to stem rust, caused by *Puccinia graminis* Pers. f. sp. *avenae* Erikss, and E. Henn., races 1, 2, 5, 8, 8A, 9, 10, and 11 in White Russian. Designated "S" by Dietz (*1928*) and "D" by Murphy and Coffman (*1961*). Griffee (*1922*), Hayes *et al.* (*1928*), Smith (*1934*), Cochran *et al.* (*1945*), Kehr *et al.* (*1950*), Myers *et al.* (*1955*), Koo *et al.* (*1955*), Koo *et al.*), (*1956*), McKenzie and Green (*1962*), Upadhyaya and Baker (*1962a*).

I-Pg-1. Dietz (*1928*). Dominant gene inhibiting the expression of Pg-1 and Pg-2, in Burt.

Pg-2. Dietz (*1928*). Dominant gene for resistance to *P. graminis* races 1, 2, 3, 5, 7, 7A, and 12 in Green Russian. Designated

[8]Personal communication.

"A" by Welsh and Johnson (*1954*). Welsh (*1931*), Gordon and Welsh (*1932*), Smith (*1934*), Torrie (*1939*), Litzenberger (*1949b*), Myers *et al.* (*1955*), Koo *et al.* (*1955*), Baker (*1955*), Koo *et al.* (*1956*), McKenzie and Green (*1962*), Upadhyaya and Baker (*1962a*). Allelic or closely linked with Pg-1 and Pg-8.

Pg-3. Waterhouse (*1930*). Dominant gene for resistance to *P. graminis* races 1, 3, 4, and 11 in Joanette. Designated "E" by Welsh and Green (*1958*). Welsh (*1931*), Gordon and Welsh (*1932*), Welsh and Johnson (*1951*), McKenzie and Green (*1962*). Allelic or closely linked with Pg-9.

Pg-4. Welsh and Johnson (*1954*). Dominant gene for resistance to *P. graminis* races 1, 2, 3, 4, 5, 6, 7, 8, 10, 11, 12, and 13 in RL1225 (derived from Hajira). Designated "B." Litzenberger (*1949b*), Welsh and Johnson (*1951*), Baker (*1955*), Upadhyaya and Baker (*1960*), McKenzie and Green (*1962*). Allelic or closely linked with Pg-13.

Pg-5. Welsh and Johnson (*1954*). Dominant gene for resistance to certain races of *P. graminis* in RL1225 (derived from Hajira). Designated "C" and may be the same as Pg-4. Litzenberger (*1949b*), Welsh and Johnson (*1951*), Baker (*1955*), Upadhyaya and Baker (*1960*), Upadhyaya and Baker (*1962a*) designated it "G."

Pg-6. Zillinsky *et al.* (*1956*). Dominant gene for resistance to *P. graminis* races 6, 7, 7A, and 8 in the diploid CD3820. Sadanaga *et al.* (*1960*), Dyck and Zillinsky (*1962*).

Pg-7. Zillinsky *et al.* (*1956*). Second dominant gene for resistance to *P. graminis* races 6, 7, 7A, and 8 in the diploid CD3820.

Pg-8. Browning and Frey (*1959*). Recessive gene for resistance to *P. graminis* races 1, 2, 6, 6A, 7, 7A, 8, 8A, 10, 13, and 13A. Designated "F" by Welsh *et al.* (*1961*). Browning and Frey (*1962*) suggested it may be allelic or closely linked with Pg-1 and Pg-2.

Pg-9. McKenzie and Green (*1965*). Recessive gene for resistance to *P. graminis* races 6F and 6AF in C.I. 4529 and other lines. Designated "H." Allelic or closely linked with Pg-3.

Pg-10. Pavek and Myers (*1965*). Dominant gene for mesothetic reaction to *P. graminis* race 13A in C.I. 1575 and other lines. Designated "G."

Pg-11. McKenzie and Martens (*1968*). Incompletely recessive gene conferring adult plant resistance to a wide range of *P. graminis* races. Derived from C.I. 3034. Independent of the Pg-2, Pg-4, and Pg-9 loci.

Pg-12. Martens, McKenzie and Fleischmann (*1968*). Recessive gene conferring seedling resistance (which changes to moderate susceptibility in the adult plant stage) to a wide range of *P. graminis* races. Derived from C.I. 8250 (cv. Kyto from Yugoslavia). Independent of the Pg-2, Pg-4, and Pg-9 loci.

Pg-13. McKenzie, Martens and Rajhathy (*1970*). Recessive gene conferring resistance to a wide range of *P. graminis* races. Derived from *A. sterilis* CAV 2647, Beja, Tunisia. Allelic or tightly linked with Pg-4.

Pg-14. MacKey and Mattsson (*1972*). Dominant or semidominant gene, carried by S 81 and other lines, that confers resistance to Swedish oat stem rust isolate Leijerstam 6AB 26-59. Designated "N."

Psc-1. Griffiths (*1961*). Partially recessive gene in Cc4146 for resistance to halo blight (*Pseudomonas coronafaciens* (Elliott) Stevens).

Psc-2. Cheng and Roane (*1968*). Gene in Dubois, linked to Psc-3, for resistance to halo blight (*Pseudomanas coronafaciens*).

Psc-3. Cheng and Roane (*1968*). Gene in Victorgrain, linked to Psc-2, for resistance to halo blight (*Pseudomonas coronafaciens*).

Pt-1. Nilsson-Ehle (*1909*). Gene for open panicle type. Designated "A_1." Norton (*1907*), Wakabayashi (*1921*), Garber (*1922*), Quisenberry (*1926*), Odland (*1928*), Coffman (*1964*).

Pt-2. Nilsson-Ehle (*1909*). Second gene for open panicle types. Designated "A_2." Quisenberry (*1926*), Coffman (*1964*).

Pt-3. Nilsson-Ehle (*1909*). Third gene for open panicle type. Designated "A_3." Coffman (*1964*).

Pt-4. Patterson *et al.* (*1959*). Dominant gene for dense or cluster panicle type in Milford.

Pt-5. McGinnis and Lin (*1966*). Gene for equilateral panicle in Garry (nullieffect and monoeffect).

pt-6. Dyck (*1968*). Recessive gene for cluster panicle in *A. strigosa*—a mutation produced by X-rays.

pt-7. Nishiyama (*1957*). Recessive gene for spear-shaped panicle in progeny of *A. barbata* x *A. strigosa.*

Px-1a. Marshall and Allard (*1969*). Slower migrating allele (Rf = 0.85) of a gene for anodal peroxidase in *Avena barbata.* Designated APX_5.

Px-1b. Marshall and Allard (*1969*). Faster migrating allele (Rf = 0.88) of a gene for anodal peroxidase in *Avena barbata.* Designated APX_5.

Px-2. Levings, Stuber, and Murphy (*1971*). Dominant gene for an auxin inducible peroxidase in certain winter oat cultivars.

Px-3a. Smith (*1972*). Active allele of a gene for peroxidase in certain oat cultivars. Designated "PA_1."

Px-3b. Smith (*1972*). Inactive allele of a gene for peroxidase in certain oat cultivars. Designated "Pa_1."

Px-4a. Smith (*1972*). Active allele of a gene for peroxidase a_1 in certain oat cultivars. Designated "PXA_1."

Px-4b. Smith (*1972*). Active allele of a gene for peroxidase a_2 in certain oat cultivars. Designated "PXA_2."

Px-4c. Smith (*1972*). Inactive allele for peroxidase in certain oat cultivars. Designated "PXa."

Px-5a. Yen (*1975*). Fast allele of a gene for peroxidase in certain oat cultivars.

Px-5b. Yen (*1975*). Medium allele of a gene for peroxidase in certain oat cultivars.

Px-5c. Yen (*1975*). Null allele of a gene for peroxidase in certain oat cultivars.

Px-6a. Yen (*1975*). Medium allele of a gene for peroxidase in certain oat cultivars.

Px-6b. Yen (*1975*). Null allele of a gene for peroxidase in certain oat cultivars.

rp-1. Henning (*1924*). Recessive gene for rachilla pubescence. Odland (*1928*), Hayes *et al.* (*1928*), Ma (*1933*), Philp (*1933*), Aamodt *et al.* (*1934*), Tang (*1938*).

Rp-2. Johnson (*1933*). Dominant gene for long, abundant rachilla pubescence. Designated "N." Coffman (*1964*).

Rp-3. Johnson (*1933*). Gene conditioning short rachilla pubescence, hypostatic to Rp-2. Designated "F."

Rp-4. Coffman (*1964*). Second dominant gene for long, abundant rachilla pubescence.

Rp-5. Nishiyama (*1933*). Gene for glabrous rachilla segment. Discovered by monosomic analysis.

sc-1. Pridham (*1916*). Recessive gene for pinkish straw color in Algerian.

Syn-1. Nishiyama (*1931*). Dominant gene for regular chromosome pairing (nullieffect). Nishiyama (*1933*), Huskins and Hearne (*1933*), Hacker and Riley (*1965*), Thomas and Mytton (*1970*).

syn-2. Dyck and Rajhathy (*1965*). Recessive gene conditioning desynapsis during meiosis in *A. strigosa.*

syn-3. Thomas and Rajhathy (*1966*). Recessive gene conditioning desynapsis during meiosis in tetraploid oats. Designated ds_2.

Syn-4. Hacker and Riley (*1965*). Dominant gene for regular chromosome pairing (nullieffect).

Syn-5. Hacker and Riley (*1965*). Dominant gene for regular chromosome pairing (nullieffect).

Tg-1. Gardenhire (*1964*). Dominant gene for resistance to *Toxoptera graminium* Rond. (Greenbug) in Russian 77.

U-1. Wakabayashi (*1921*). Dominant gene for resistance to covered smut, caused by *Ustilago kolleri* Wille., in Red Rustproof. Gains (*1925*), Nicolaisen (*1931*), Schattenberg (*1934*).

U-2. Wakabayashi (*1921*). Second dominant gene for resistance to *U. kolleri* in Red Rustproof. Gaines (*1925*), Nicolaisen (*1931*), Schattenberg (*1934*).

U-3. Wakabayashi (*1921*). Third dominant gene for resistance to *U. kolleri* in Red Rustproof. Gaines (*1925*), Schattenberg (*1934*).

U-4. Barney (*1924*). Dominant gene for resistance to loose smut, caused by *Ustilago avenae* (Pers.) Rostr., in Black Mesdag. Reed (*1925*), Reed (*1928*), Garber *et al.* (*1928*), Garber *et al.* (*1929*), Rosenstiel (*1929*), Nicolaisen (*1931*), Johnson (*1933*), Stanton *et al.* (*1934*), Reed (*1934*), Schattenberg (*1934*), Reed (*1935*), Reed (*1941*), Cherewick and McKenzie (*1969*).

U-5. Barney (*1924*). Dominant gene for resistance to *U. avenae* in Fulghum.

U-6. Barney (*1924*). Second dominant gene for resistance to *U. avenae* in Fulghum. Cochran *et al.* (*1945*).

U-7. Barney (*1924*). Dominant gene for resistance to *U. avenae* in Burt.

U-8. Barney (*1924*). Second dominant gene for resistance to *U. avenae* in Burt.

U-9. Barney (*1924*). Dominant gene for intermediate reaction to *U. avenae* in Golden Rain.

U-10. Reed (*1928*). Dominant gene for resistance to *U. kolleri* in Early Gothland. Reed (*1931*), Reed and Stanton (*1937*).

U-11. Reed (*1928*). Dominant gene for resistance to *U. avenae* in Monarch. Reed (*1931*), Schattenberg (*1934*), Reed (*1941*).

U-12. Gaines and Smith (*1929*). Gene for resistance to *U. kolleri* in Markton. Coffman *et al.* (*1931*), Schattenberg (*1934*), Reed and Stanton (*1938*), Cherewick and McKenzie (*1969*).

U-13. Gaines and Smith (*1929*). Second gene for resistance to *U. kolleri* in Markton. Coffman *et al.* (*1931*), Schattenberg (*1934*), Reed and Stanton (*1938*).

U-14. Nicolaisen (*1931*). Dominant gene for resistance to *U. avenae* in Black Mesdag. Johnson (*1933*), Schattenberg (*1934*).

U-15. Nicolaisen (*1931*). Second dominant gene for resistance to *U. avenae* in Black Mesdag. Schattenberg (*1934*).

U-16. Schattenberg (*1934*). Dominant gene for resistance to *U. avenae* in Markton. Reed and Stanton (*1938*).

U-17. Schattenberg (*1934*). Gene for resistance to *U. avenae* in Gopher.

U-18. Reed and Stanton (*1937*). Gene for resistance to *U. kolleri* in Rossman.

U-19. Reed and Stanton (*1937*). Gene for resistance to *U. kolleri* in Danish.

U-20. Reed and Stanton (*1937*). Gene for resistance to *U. kolleri* in Scottish Chief.

U-21. Reed and Stanton (*1937*). Gene for resistance to *U. kolleri* in Seizure.

U-22. Hayes *et al.* (*1939*). Gene for resistance to *U. avenae* and *U. kolleri* in Bond. Torrie (*1939*), Cochran *et al.* (*1945*).

U-23. Torrie (*1939*). Gene for partial resistance to *U. avenae* and *U. kolleri* in Bond.

U-24. Torrie (*1939*). Gene for resistance to *U. avenae* and *U. kolleri* in Victoria. Patel (*1941*), Cochran *et al.* (*1945*), Cherewick and McKenzie (*1969*).

U-25. Torrie (*1939*). Gene for partial resistance to *U. avenae* and *U. kolleri* in Victoria.

U-26. Reed (*1942*). Gene for resistance to *Ustilago* species in Navarro. Narain (*1966*).

U-27. Reed (*1942*). Gene for resistance to *Ustilago* species in Navarro. Narain (*1966*).

U-28. Reed (*1942*). Gene for resistance to *Ustilago* species in Navarro.

U-29. Reed (*1942*). Gene for resistance to *Ustilago* species in Navarro.

U-30. Reed (*1942*). Gene for resistance to *Ustilago* species in Navarro.

CATALOGING AND SYMBOLIZING GENES DISCOVERED IN THE FUTURE

We propose that we continue to serve as a committee, and that we catalog genes in oats that are discovered and reported in the future. Investigators wishing to have new genes cataloged would send pertinent data to a member of the committee. The committee will then see that the symbols assigned do not duplicate previous symbols. We further propose that new genes be listed annually in the *Oat Newsletter*.

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